

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 5 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 10 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 20 Ser Val Gly Ser Gly Glu Thr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Glu Asp Val Ala Val Leu Glu Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 25 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Glu Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Glu Glu Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 35 Thr Gly Ala Glu Glu Thr Leu Asn His Leu Ile Glu Phe Asp Ala Ala
 690 695 700
 Ile Glu Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly Glu
 705 710 715 720
 40 Val Val Gly Met Asn Thr Ala Ala Ser
 725

 45 <210> SEQ ID NO:10
 <211> 1797
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: chi-fusion
 protein TDH9-RN35 (designated Mrb58f)
 <222> (1)..(1791)

 cat atg cat cac cat ctc cat cac atg gtc gat ttc ggg ggg nta one 48
 His Met His His His His His His Met Val Asp Phe Gly Ala Leu Pro
 55 1 5 10 15

 cag gag atc acc tcc ggc agg atg tac gac ggc ccc ggt tgg gca tgg 56
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
 20 25 30

 60 ctt gtt gtc gct gct gct cag aag tgg gac agc gtg ggg aat gac ctc ttt 144
 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 25 30 45

 65 tgg gcc ggc tgg tgg tcc cag tgg gtc tgg aat ctt aat gtc ggg 192
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 30 35 40

tcc tgg cta ggt tag tgg gag ggt ctc atg stg stg ggc ggc gac tag cod 240
 Ser Trp Ile Gly Ser Ser Ala Gly Ileu Met Val Ala Ala Ala Ser Pro
 49 70 75 80
 5 tat gag ccc tgg stg aac gtc acc gag gag gag gag gag cod acc goc 284
 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Ser Ala Glu Leu Thr Ala
 85 90 95
 10 gcc cag gtc cgg gtt gct gac gag gag gag gag gag gag tat ggg ctg 336
 Ala Glu Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 100 105 115
 15 acg gtc ccc ccc cod gtc acc gac gag acc cgt gct gaa ctg atc gtc 384
 Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Ileu Met Ile
 115 120 125
 20 ctg atc gog acc aac atc ttg ggg cca aac acc ccc gag gag acc goc gtc 432
 Leu Ile Ala Thr Asn Leu Gly Glu Asn Thr Pro Ala Ile Ala Val
 130 135 140
 25 acc gag gac gac tac ggc gag tag tag gac gac gac gac gac atc 480
 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Glu Asp Ala Ala Met
 145 150 155 160
 30 25 tat agg tcc gac gac gag acc acc gag gag gag gag gag tcc ctg cod 528
 Phe Val Tyr Ala Ala Thr Ala Thr Ala Thr Ala Leu Leu Pro
 165 170 175
 35 ttc gac gac gac gac gag acc acc agg gag gat ggg atc ctc gag cod 576
 Phe Glu Glu His Pro Glu Met Thr Ser Ala Gly Gly Ileu Leu Glu Glu
 180 185 190
 40 gcc gcc gcc gtc gag gag acc acc gac gac gac gac gag gag gag 624
 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr His Ala Ala Asn Glu Leu
 195 200 205
 45 atg aac aat gtc ccc ccc gag gag ctg cca gag gag ctg gag gag gag 672
 Met Asn Asn Val Pro Glu Ala Ileu Glu Glu Leu His Glu Pro Thr Glu
 210 215 220
 50 gac acc 720
 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
 225 230 235 240
 55 atg tat atg atg acc 768
 Met Ser Met Thr Asn Ser Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
 245 250 255
 60 atg thg aac ggc ctr got ccg gag gag gag gag gag gag gag gag gag 816
 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Glu Glu Val Glu Ser Thr
 265 270
 65 gct tcc tat ggt ctg gag ggt ggg gtc gag gag gag gag gag gag 864
 Ala Ala Glu Asn Val Arg Ala Met Ser Ser Lys Glu Ser Ser Leu
 275 280 285
 70 ggt tct tat ggt ctg gag ggt ggg gtc gag gag gag gag gag gag 912
 Gly Ser Ser Gly Leu Gly Gly Val Ala Asn Leu Lys Arg Ala
 290 295 300
 75 gac tat gtc ggt tat ttg tag gtg ccc gag gac gac tat ggg gac 960
 Ala Ser Val Gly Ser Leu Ser Val Pro Glu Ala Trp Ala Ala Asn
 305 310 315
 80

cag gca gtc acc cug gcg gac ggg ctc cog cog acc acc aac 1055
 Gin Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
 340 345 350

5 agc gcc ggc gaa aga ggg ccc ggg cog amg ctg egg ggg ctc cog gtc
 Ser Ala Ala Glu Arg Gly Pro Gly Gin Met Leu Gly Leu Pro Val
 365 370 375

10 ggg cag atg ggc gcc agg gcc aat ggt ggg ctc aat gtc ctc cog
 Gly Glu Met Gly Ala Arg Ala Gly Gly Ieu Ser Gly Val Leu Arg
 376 378 380

15 gtt ccc cgg ccc ttc ttc aat ggg cat ttc cog gca acc ggc gag
 Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
 386 390 394

20 atc gac ccc ccc gcc ttc tcc tcc ccc gag egg ttc gcc gag ttc ccc ggg
 Ile Ala Pro Pro Ala Ieu Ser Glu Asp Arg Phe Ala Asp Phe Pro Ala
 405 410 415

25 ctc ccc ctc gag ccc tcc gag aat gtc gag ccc gtc ggg ccc ccc gtt
 Ieu Pro Leu Asp Pro Ser Ala Met Val Ala Glu Val Gly Pro Ser Val
 420 425 430

30 gtc acc acc acc aac atg ggc tcc aac acc acc gtc gtc aac ggc ggg
 Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ile Gly
 435 440 445

35 acc ggc acc gtc acc acc acc ggc acc gtc ggg ctc acc acc acc acc
 Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
 450 455 460

40 gtc acc acc acc aac atc gag acc aat gag ttc aat aat gtc ggc acc
 Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
 465 470 475

45 ccc acc tcc ggc gtc gag gtc gtc egg tat gag cog acc acc gag gtc
 Glu Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Glu Asp Val
 480 490 495

50 ggc gtc ctg ccc ctg ccc gag gtc ggc acc ccc gag cog cog tcc
 Ala Val Leu Glu Ieu Arg Gly Ala Gly Ile Ieu Pro Ser Ala Ala Ile
 505 508 510

55 ggt gpc ggc gtc aag gtc ggt gpc gac gcc gtc ggg aty ggc aac aac
 Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asp Ser
 515 520 525

60 ggt ggg ccc ggg gaa aac ccc ccc ggg gtc gcc ggg aag gtc gtc pog
 Gly Gly Glu Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
 530 535 540

65 ctc pog ccc aac gag ccc gag ggg tcc gag tcc gag tcc acc gtc gtc ggg
 Leu Gly Glu Thr Val Glu Ala Asp Ser Ieu Thr Gly Ala Glu Glu
 555 560 565

70 acc aac ggg tcc aac ccc tcc gag tcc gag tcc gag aac ccc gag gag
 Thr Leu Asn Gly Leu Ile Glu Phe Asp Ala Ile Glu Pro Gly Asp
 566 570 575

75 tcc ggg ggg acc gtc gtc aac ggg ctc aac ccc gag ggg gtc ggt atg aac
 Ser Gly Gly Pro Val Val Asn Gly Ieu Gly Glu Val Val Gly Met Asn
 580 585 590

80 aac gcc ggg tcc taggatata
 thr Ala Ala Ser
 595

1797

<210> SEQ ID NO:20
 <211> S96
 <212> PFT
 5 <213> Artificial Sequence
 <214> Description of Artificial Sequence: bi-fusion
 protein TDKS-Ka5 (designated Mtb595)

 His Met His His His His His Met Val Asp Phe Gly Ala Leu Pro
 10 1 5 10 15
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
 20 25 30
 15 Ile Val Alz Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45
 Ser Ala Ala Ser Ala Phe Glu Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60
 20 Ser Tyr Ile Gly Ser Ser Ala Gly Ile Met Val Val Ala Ala Ala Ser Pro
 65 70 75 80
 25 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
 85 90 95
 Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 105 110 115
 30 Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Gln Leu Met Ile
 115 120 125
 Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
 130 135 140
 35 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
 145 150 155 160
 40 Phe Gly Tyr Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu PRO
 165 170 175
 Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Glu
 185 195 200 205
 45 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Glu Leu
 195 200 205
 Met Asn Asn Val Pro Glu Ala Leu Glu Gln Leu Ala Glu Pro Thr Gln
 210 215 220
 50 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
 225 230 235 240
 Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
 245 250 255
 55 Met Ser Met Thr ASN Ser Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
 260 265 270
 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Glu Thr
 275 280 285
 Ala Asn Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
 290 295 300
 60 Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
 305 310 315 320
 Ala Ser Val Gly Ser Leu Ser Val Pro Glu Ala Ala Trp Ala Ala Asn
 325

	325	330	335
Sir	Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr		
5	340	345	350
Ser	Ala Ala Glu Arg Gly Pro Gly Glu Met Leu Gly Glu Leu Pro Val		
	355	360	365
Gly	Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg		
10	370	375	380
Val	Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp		
	385	390	395
Ile	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala		
15	405	410	415
Leu	Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val		
	420	425	430
Val	Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly		
20	435	440	445
Thr	Gly Ile Val Ile Asp PRO ASN Gly Val Val Leu Thr Asn Asn His		
25	450	455	460
Val	Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly		
	465	470	475
Gln	Thr Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val		
30	485	490	495
Ala	Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile		
	505	510	515
Gly	Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser		
35	525	530	535
Gly	Gly Glu Gly Gly Thr Pro Asp Ala Val Pro Gly Arg Val Val Ala		
40	535	540	545
Leu	Gly Glu Thr Val Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu		
	545	550	555
Thr	Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp		
45	555	570	575
Ser	Gly Gly Pro Val Val Asn Gly Leu Gly Glu Val Val Gly Met Asn		
	580	585	590
Ter	Ala Ala Ser		
	595		

55 (a) INFORMATION FOR SSO ID NO:21: DPV GHTB9.0

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDBEHAVIOR: single
(D) TOPOLOGY: linear

(x4) SOURCE DESCRIPTION; SEQ ID NO:21;

卷之三
五
240

ACAGTACATC GGGCTTTCG AGTCTGGTTGC CGGCTCTTCG AACAACTATT AGGGCCATTC	300
GCGGCTTCA CGGGGACCCG GGTCTTCCC CGGGCTTGC CGGGCTTCC CGGGCTTCA	360
ACGGGCGGA TCCCGAACCG CGGGGCGGA CGGGGCGGA CGGGGCGGA CGGGCTTCA	420
CGGGGCGGA CGGGCTTGC CGGGCTTGC CGGGCTTGC CGGGCTTGC CGGGCTTCA	480
CGGGGCGGA CGGGCTTGC CGGGCTTGC CGGGCTTGC CGGGCTTGC CGGGCTTCA	540

5

(2) INFORMATION FOR SEQ ID NO:22: DPP (MTB9.4)

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro	
1 5 10 15	
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gin Val Val Ala	
20 25 30	
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gin Phe Asn Ala Ser	
35 40 45	
Pro Val Ala Glu Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro	
50 55 60	
Gly Arg Ala Ala Met Ala Ala Glu Leu Glu Ala Val Pro Gly Ala Ala	
65 70 75 80	
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr	
85 90 95	

30

(2) INFORMATION FOR SEQ ID NO:23: MBL (MTB9.5)

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGTTCCGA TAGCTGTTTC GCGGCTTCTGA CGGGGCTTCA CGGGCTTCTGA CGGGCTTCTGA	60
CGGGCTTCTGA GACGGCTTCA TGGGGCTTCA CGGGCTTCA AGGGCTTCTGA GTGGGGGGGG	120
TGGGGCTTCA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA	180
CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA	240
GAGGGCTTCA CTTACCCAC GAGGGCTTCA ACCGGGTTCA CGGGCTTCTGA CGGGCTTCTGA	300
GCTGGCTTCA GAGGGCTTCA ATGGGGCTTCA TGGGGCTTCA TGGGGCTTCA TTGGGGGGGG	360
CGGGCTTCTGA TTGGGGGGGG GAGGGCTTCA TGTTGGGGGG CGGGCTTCTGA CGGGCTTCTGA	420
AGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA	480
CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA	540
CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA CGGGCTTCTGA	600

60

(2) INFORMATION FOR SEQ ID NO:24: MBL (MTB9.6)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ser Leu Leu Asp Ala His Ile Pro Glu Leu Val Ala Ser Glu Ser
 1 5 16 18
 5 Ala Phe Ala Ala Lys Asn Gly Leu Met Arg His Thr Ile Gly Glu Ala
 10 20 26 30
 Glu Glu Ala Ala Met Ser Ala Glu Ala Phe His Glu Gly Glu Ser Ser
 35 40 45
 Ala Phe Glu Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Ieu Asp Val Ala Glu Ala Asn Leu Gly Glu Ala Ala
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 15 Phe

(2) INFORMATION FOR SEQ ID NO:25: MTI (NTB9.PA)

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) ORIGINAL SOURCE:
 (xii) ORGANISM: *Mycobacterium tuberculosis*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGTCCTTCTT	TCACGTGAA	AAGTTGGTG	GCCCCAGTGG	CCGCGGCGC	ATATGGGCC	50
ATATCGCGG	GTCCCTGAA	TGCTCCGAA	GCACGCGCT	AGACGCGATC	AGGCGCGACG	120
35	CTGCGGACA	CTACGCGGC	CAACGCGTC	CTCGCGCGCT	TCTCGCGAT	180
TCTCGAGGT	CTGTAAGGC	TTCGAGACT	GCGACGTCG	GGCGCGCGCG	GGACGCGGG	240
GAAGCGCTG	5CGCGCGCG	CGCGCGCGG	CGCTGCGACA	CCCGCGATTC	GAGATGCGG	300
CGATGCGAC	GTGCGCTGAC	ATCGCGCGA	GTCTCGATCT	ACCGCGCGCC	GAGCGCGG	360
40	ATGTCGTCG	TCGCGCGCG	TCGCGCGCG	ATCGCGCGCG	ACGCGCGCG	420
CTGAGCGCG	CGATCGCGC	CGATCGCGC	CGATCGCGC	CGATCGCGC	CGATCGCGC	480
CGCGCGCG	CGCGCGCG	TCGCGCGC	TCGCGCGC	GGATCGCG	GGATCGCG	540
TGCTGGGG	CGACGCGCG	TCGCGCGCG	TCGCGCGCG	GGATCGCGT	ACACGCGCG	600
50	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	GGATCGCGT	GGATCGCGT	660
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	720
CTCGACGTC	CGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	780
60	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	840
CGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	900
ACCGCGCGT	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	960
ACGATTCAC	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1020
55	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1080
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1140
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1200
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1260
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1320
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1380
60	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1440
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1500
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1560
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1620
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1680
TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	TCGCGCGCG	1740

65 (2) INFORMATION FOR SEQ ID NO:26: MTI (NTB9.PA)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2836 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (i) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTGATGTCG	TTCGGGGCG CGCCAGAACG CACCAACTCC	GCCTGGGGGC TCGACGAGG	60
GTTGCGCTTG	GTGCGCGCG CGAACTCCCGA GATGCGTGG	CTGCTGGCGG TTGCTGGGGT	120
CGATACCG	CACGGATCGG AGCGCGATCG TTGCTGGGGT	CGCTCGGGCG TACTTGGCGA	180
15 CGACGATCG	CGCGTTTTT AGCTCGATCG CGCGCGCGT GACGTTGGCG	CGACGGGGCA	240
CGACGCTTG	CGTGGGGCGG CGCGCGCGAT CGACGCGATCG	CTGCTGGGGG	300
GCCTGGGGGT	GTGGGGGGCGG CGCGCGCGAT CGACGCGATCG	CGCGCGCGGT CGCGCGCGGT	360
CGATTTGG	CGTGGGGGGCGG CGCGCGCGAT CGACGCGATCG	CGCGCGCGGT CGCGCGCGGT	420
20 CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	AGCGCGCGAT CGTGGGGCG	480
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	ATACGCGTGG	540
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	600
25 CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	660
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	720
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	780
30 CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	840
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	900
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	960
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1020
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1080
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1140
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1200
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1260
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1320
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1380
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1440
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1500
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1560
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1620
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1680
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1740
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1800
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1860
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1920
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	1980
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2040
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2100
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2160
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2220
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2280
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2340
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2400
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2460
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2520
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2580
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2640
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2700
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2760
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2820
CGACGCGGG	CGACGCGGG CGACGCGATCG AGCGCGCGAT CGACGCGATCG	CGACGCGGG CGACGCGGG	2880

60 (2) INFORMATION FOR SEQ ID NO:27: MTI (MTB9.5A)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

5 (iv) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Glu Ala Met	1 5 10 15
Ile Arg Ala Leu Ala Gly Ieu Leu Glu Ala Glu His Glu Ala Ile Ile	20 25 30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Glu Ala Gly Ser Ala	35 40 45
Ala Cys Glu Gly Phe Ile Thr Glu Leu Gly Arg Asn Phe Glu Val Ile	50 55 60
Tyr Glu Glu Ala Asn Ala His Glu Glu Lys Val Glu Ala Ala Gly Asn	65 70 75 80
Asn Met Ala Glu Thr Asp Ser Ala Val Glu Ser Ser Trp Ala	85
	86 89

(2) INFORMATION FOR SEQ ID NO:28: MTCM1

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGCTTGG CAGAGGTTTC ATCAGTCATC GAGACATGAG TGGCATGAGC GGCTTGTAAC	69
ACCTTGTGG GATTGTTATA CCTAACCAAGG GGGTGTACCTT TTAATCTCTCA CTGAGTACT	120
TGAAATTAAGG CCTTGAGGCG CCTTGAGGCG GTTGTGCGG GTAGAGTGTTG TGATGTTGCG	180
GCGGGACAA ATACGGCGCC PAAACCGGCA ACCGGTGTAA TTITTTTCAG GAACTGGCAG	240
ATGCTTGTG TTGGCTGCTC AGGCTTGAATC AGGCGAGGC CAAAGGGGTC CAAAGGGGCC	300
GGAGACATCT GGAGGGGCGC AAAGGAGGTC TGAGGTGTTG GGGGGGGGCG GTGTTGGAGC	360
TGAGCTTACAT CGCGGCTGTC GGGGAGGCGC TATGGCGCGG CTTTGAGGGG CGTTTTGGG	420
CGGGGGGGAT GGGGGGGGGG GGGGGGGGGG TTGGTGTACTT GTCGTTAAAG AGGTTTATCGA	480
AGGGAGCTAT ACTGGCTTCA TGCTGGTCCC AATTTGGGAA GTTGGGGCGG GGGGGGGGGT	540
CGAACATCAT TTGGAGTOTO GCGGAGATCA TCAAGGCGAC CCTTGAGAGA GTTGGGGAGT	600
TGTACCAA GCGGTCACAC GGGCTTAAGG AGCTTGGGGG GAACTGAGG GTTGGGGTGA	660
CGGGCTTTT CTCTGAGGAGG TGGTGGAGC TGGATGCTT CTTGGGGGGC GTCCGGGGT	720
TGACGGGCGC GACCGGGCGC TTGGTGGAGC TGAATGGCTT TTGGGGGGG GCGGGTCTAT	780
CGGGGGGGAT GGGGGGGGGG GGGGGGGGGG CTGGGGGGGG GGGGGGGGGG TTGGGGGGGG	840
GG	900
GG	960
AGGG	1020
GG	1080
AGTATCTGGA AGGGGGGGGG GGGGGGGGG GGGGGGGGG GGGGGGGGG GGGGGGGGG	1140
GG	1200

55 (2) INFORMATION FOR SEQ ID NO:29: MTCM1

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15
 Leu Tyr Asp Ile Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30
 5 Tyr Ser Ser Leu Glu Tyr Phe Glu Cys Ile Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 Gly Lys Asn Arg Asn His Val Asn Phe Glu Glu Leu Ala Asp Ileu
 65 70 75 80
 Asp Arg Glu Leu Ile Ser Leu Ile His Asp Glu Ala Asn Ala Val Glu
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 15 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Glu Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 135 140 145
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 155 160 165
 Thr Glu Leu Leu Lys Leu Ala Iys Leu Ala Glu Leu Val Ala Ala
 175 180 185
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 190 195 200 205
 25 Leu Gly Glu Val Trp Glu Phe Ile Tyr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Ala Glu Val Pro Gly Leu Thr
 225 230 235 240
 30 Gly Ala Thr Ser Gly Leu Ser Glu Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 35 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Glu Val His Ala Ala Ser Thr Arg Glu
 290 295 300
 40 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Glu Glu
 305 310 315 320
 Val Gly Gly Glu Ser Glu Leu Val Ser Ala Glu Gly Ser Glu Gly Met
 325 330 335
 Gly Gly Pro Val Gly met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 45 Lys Gly Thr Thr Thr Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Glu
 370 375 380
 50 Lys Val Leu Val Arg Asn Val Val
 385 390

(2) INFORMATION FOR SEQ ID NO:30: MTCCW2

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: cDNA
 (iii) SEQUENCE DESCRIPTION: SEQ ID NO:30:
 65 GCGATGTTTGTGAGTTTTCGGGGTTTACCTGGGAA GTGATTTCAA GCGGAATGTA
 TCCGGTCCG GGGCCGGTGT CGATGTTACG CGCCCGCGCCG GCGCTGGACG GGGTGCGGC
 AGGGTTTACT CGCGCGCGC TGCTGATGTC ATGGGGTGCG CGCGAGGCTGA TTGTGAGCC
 CGTGGATGGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 70 75 80
 120 125 130
 180 185 190
 240 245 250

(2) INFORMATION FOR SEQ ID NEX-132: MWGCGAG

25 (ii) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 423 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) POLYMER: linear

30

(ii) MOLECULE TYPE: protein

EX-14 BUSINESS DESCRIPTION: SMC ID NO:31,

	Met	Asp	Thr	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr	
															10	15	
	i																
	Ser	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Trp	Ksp		
40	Gly	Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Ala	Val	Ser	Tyr	Gly	Ser	
															35	40	
	Val	Ser	Thr	Ile	Ile	Val	Glu	Pro	Tyr	Met	Gly	Pro	Ala	Ala	Ala		
															50	55	
45	Met	Ala	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Ieu	Ala	Ala		
															65	70	
	Ala	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Glu	Ala		
															85	90	
	Phe	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala	
															100	105	
50	Asn	Arg	Ser	Arg	Leu	Met	Ser	Lys	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln	
															115	120	
	Asn	Ser	Ala	Ala	Ile	Kin	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Gln	Gln	Met	Tyr
															135	138	145
55	Ala	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Gly	Gly	Ala	Ser	Ala	Ala	
															145	150	155
	Ala	Ser	Ala	Leu	Pro	Phe	Thr	Pro	Val	Gly	Gly	Thr	Gly	Pro		165	170
															185	190	195
60	Ala	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly		
															195	200	205
	Leu	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Ile	Thr	
															215	220	225
65	Ser	Gly	Leu	Ieu	Gly	Ala	Ser	Thr	Leu	Asn	Pro	Gly	Val	Gly	Ser		
															235	240	245
	Ala	Gly	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile	
															255	258	265
	Ala	Leu	Tyr	Ile	Ala	Ser	Ile	Kis	Thr	Gly	Gly	Ile	Ala	Leu	Ala	Ile	

260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Ieu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gin Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335 340
 10 Thr Thr Thr Ala Aln Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Ieu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Glu Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Glu Pro
 405 410 415
 20 Pro Pro Gly Asn Pro Phe Arg
 420

(2) INFORMATION FOR SEQ ID NO:32: E8AT-6

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

35 ATGACAGGGAAAGTTTCGCGGATGTCAGGCGGCGGACAGGAAATGCAAGGA
 ANTGCAGTGGGGATGGCTTGACGGATTCAGGAGGAGTCCCTGAGCAGAGCTGGCA
 60 CGGGCTGGG GCGGTAGCGG TTGGAGAGCG TACG
 120
 134

(2) INFORMATION FOR SEQ ID NO:33: E8AT-6

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

50 Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ser
 1 5 15 19
 Ala Ile Glu Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20 25 30
 Lys Glu Ser Leu Thr Lys Leu Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 Glu Ala Tyr
 50

(2) INFORMATION FOR SEQ ID NO:34: Th38-1

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGGCAAGAAGA	GACCGTTCGGC	GCTACCCCT	CGCGGAGGAGC	AAGTATTTTC	GGGGAGATCT	60
CGGGGACTT	GAALAKCCCC	ATGCCACGGG	TGGATGAGC	GGCAGGTTTG	TGGCAAGVCC	120
AGTCGCGGG	CGCGGGGGG	ACGSCCGCCC	AGCGCGGCGT	GTTGGCGTC	CAAAACGAGC	180
CGATTAATCA	GAAGCAGGAA	CTGGAGAAGA	TCTCGAGA	TATTCGTTAG	GGCGGGGTCC	240
AAATCTCGAA	GGCGCGGAG	GACGCGAAC	AGCGCTTC	CTCGGGATG	GGCTTCCTGAC	300
CGCTTATAC	GUAAAAGAAC				GGGGGAA	327

(2) INFORMATION FOR SEQ ID NO:35: Tb88-1

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Asp Ala Ala Thr Leu Ala Glu Ala Gly Asn Phe Glu Arg Ile						
1	5	10	15			
Ser Gly Asp Leu Lys Thr Glu Ile Asp Glu Val Glu Ser Thr Ala Gly						
20	25	30				
Ser Leu Glu Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Glu Ala						
35	40	45				
Ala Val Val Arg Phe Glu Ala Ala Asn Lys Glu Lys Glu Glu Leu						
50	55	60				
Asp Glu Ile Ser Thr Ala Ile Arg Glu Ala Gly Val Glu Tyr Ser Arg						
65	70	75	80			
Ala Asp Glu Glu Glu Glu Ala Leu Ser Ser Glu Met Gly Phe						
85	90	95				

(2) INFORMATION FOR SEQ ID NO:36: TbRa8

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGATTCCK CGGAGGTTA TCGACATCTT CCGGGCGGC	CCACACGTT GGAGACAGGC	60
GGCGGCGGG AGCGTCGACG CGGGCGGGAG TACGGCGGG	GGACCGGGCG CGCGCTGGGT	120
CATTGAGG CGATCGGGCG TTAACAGGGG CGGCGGAGT	ACCTGGCGCA TGAAGCTGAA	180
ATGTTGTTT AGATGGTGGC CGGGCGGGCG CGGCGGAGC	GGCGGGCGAA GGAGAGCGCA	240
AAATTCGAGG GTTTCGGGTTT GATTCGCGGG TTTCGGCGA	TCTCGCGGA GGCTTACCG	300
GGCGGGCGCA GGTCGCGGG CTGGCTGGAT CGGGCGGTC	TGGCGATTCG GGCGGGCGAC	360
CGGGCGGGCA TTTCTGGGTTT CGGGCGGGCA TGGGGGGG	GGCGGGCGGG TGCGGGGGAA	420
CGTGGCGGG CGGGCGGGCG CGGGGGGGT CGGGGGGGC	GGGGGGGGGG TGATGGGATTA	480
ACGCTGGTAA GGCGGGGGT CGGGGGGGT CGGGGGGGC	GGGGGGGGGG TGATGGGATTA	540
GGG		542

(2) INFORMATION FOR SEQ ID NO:37: TbRa1

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Ala Ala						
1	5	10	15			
Ala Glu Ala Val Glu Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val						
20	25	30				

Ala Arg Val Ile Glu Glu Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 15 40 45
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50 55 60
 5 Pro Arg
 65

(2) INFORMATION FOR SEQ ID NO:38: 38 NT

- 10 (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20	TTTTCCTGCA CGGGACGCTG GTCGAGGAAAC GCGGCCCGCGA ACGCGCTGTCG TCTCTGCCTA	65
	ACGATCGGGA AACCGCGCGA TAGCTGGCG GACTGTGCGG GUAAGTCGAG GAGGCGCGAG	125
	GCGGAATTG AGAGGACGCG AAGNGTATGGC CTGAGAATTG CTTTGCGATA CCTCTGGCG	185
25	CCTGTTGCGC GCTGGCGCCG TCTCTGAGC ACGCGCGCG TGTGCGCGA GACCACCG	245
	CGTTTCCCT GAAACCGCGG CGCGCGCGCG TACTGTGCGC ACTACCGCG CGTGTGCGC	305
	GTTGACGTTT CGCGAGCGCG GTAGCGCGCT GTCTGCGCG CGTGGGGTCC	365
30	GGCTTCTAC GAAGGTGATC CGAACGTTAC GATCGCGCGT CGAGCGCG CGTCTGGCGC	425
	CGGAGATCGG CAGGCGCGCG CGGGAGCGT CRACATGGCG GCGTGGCGCG CGTATCGCG	485
35	GGAAAGTTAT ATGGCGCGCG ACGAGGCGCT GATCGACGTC GCGCTGCGCG TGTGCGCTA	545
	GCAGGTCACG TACACCGCGC CGGAGGTTAC CGAGCGCGTC AAGCTGACG GAAAGTCCT	605
40	GGCGCGCGT TACCGAGCGA CGTCTGAGAC CGTGTGCGAC CGCGAGCGCG AGCGCGCG	665
	CGCGCGCGT AAGCTGCGCG CGCGCGCGCG AGTGGCGCTG CGCGCGCGCG AGCGCGCG	725
	TGAGCGCGTC TTGTTGCGCG AGTACGCGCG CGAGCGCGCG CGCGCGCGCG CGCGCGCG	785
45	CGCGCGCGCG CGACGCGCGCG TGAGCGCGCG CGTGGGGCGT ATAGCGCGCG	845
	CGACGCGCGCG ATGGTGGCGCG GTTGGCGCGCG GACGCGCGCG CGCGCGCGCG CGCGCGCG	905
50	CGCTTCTGCG CGGCGCGCGCG CGTGGGGCGT ATAGCGCGCG CGCGCGCGCG CGCGCGCG	965
	CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCG	1025
55	GAATGATCGAC CGACGCGCGCG CGTGGGGCGT GAAAGCGCGCG AGCGCGCGCG	1085
	GAACGCGCGCG CGCGCGCGCG CGTGGGGCGT GAAAGCGCGCG AGCGCGCGCG	1145
60	CGACGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCG	1205
	CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCG	1265
65	CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCG	1325
	CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCG	1385
	CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCG	1445
	CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCG	1505

ACCAUCCAATGCAAGGAA CACCTAACCGC GAAACCCCTTG TCAACGACGC CGTGGCCTTC 1860
 CGGTGGGGCG CTACTACCGG GGGTTGGCGC TTAATCTCCG CACCTCTGGG AGCTTGGAA 1820
 5 TCCCGCTGAT CATGCCGCGT CGGCTCTCTG TGAAGGCGC OCTGGTGATC GTGGAAAGGC 1680
 TGCGAAGG CGTGCGCG AGCTAAGGAA TATGGCTGAA ATTCCTGCG CGATACCGA 1746
 10 GCCTGCGTGT CGTTTGTGCG CGGCGAATTA CGTCGCGCC GTTCTCTCTG CATCACATG 1600
 CGCGCTGTTG CGCTCGAACG CGCTCGCGTG TCCCGCTGTG AAATCTGCG CGGGGCGT 1860
 CGGCGAAGG CGAAGGCGTG TTATGGTGG CGCTGGTGTG CGCGCTGTG GTGGTCCG 1920
 15 TTATCGCGAC CGCGCTGTG CGGCTGGTGC CGCGCTGGC CGTGGTGGC CGGGAGGCG 1980
 CGATCGGAA TTC 1993

20 (2) INFORMATION FOR SEQ ID NO:39: 38 KD

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:39:

30	Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro			
	1	5	10	15
	Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser			
	20	25	30	
35	Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser			
	35	40	45	
40	Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu			
	50	55	60	
	Phe Asn Leu Tyr Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr			
	65	70	75	80
45	Ile Thr Ala Glu Gly Thr Gly Ser Gly Ala Gly Ile Ala Glu Ala			
	85	90	95	
	Ala Glu Thr Val Asn Ile Glu Ala Ser Asp Ala Tyr Leu Ser Glu Gly			
	100	105	110	
50	Asp Met Ala Ala His Iys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser			
	115	120	125	
	Ala Glu Glu Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys			
55	130	135	140	
	Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Asn Gly Thr Ile Lys Thr			
	145	150	155	160
60	Tyr Asp Asp Pro Glu Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro			
	165	170	175	
	Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr			
	180	185	190	
65	Phe Leu Phe Thr Glu Tyr Leu Ser Lys Glu Asp Pro Glu Gly Trp Glu			
	195	200	205	

Lys Ser Pro Gly Phe Gly Ile Thr Val Asp Phe Pro Ala Val Pro Gly
210 215 220
 5 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Glu Ala
245 250 255
 10 Ser Glu Arg Gly Leu Gly Glu Ala Glu Leu Gly Asn Ser Ser Gly Asn
260 265 270
 Phe Leu Leu Pro Asp Ala Glu Asn Ser Ile Glu Ala Ala Ala Glu Phe
275 280 285
 15 Ala Ser Lys Thr Pro Ala Asn Glu Ala Ile Ser Met Ile Asp Gly Pro
290 295 300
 20 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
305 310 315 320
 Asn Arg Glu Lys Rep Ala Ala Thr Ala Glu Thr Leu Glu Ala Phe Leu
325 330 335 340
 25 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Glu Val
340 345 350
 His Phe Glu Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
355 360 365
 30 Ile Ala Thr Ile Ser Ser
370

35 (2) INFORMATION FOR SEQ ID NO:40: DPWF

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 999 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x4) SEQUENCE DESCRIPTION: SEQ ID NO:40:

45 ATGCAATCC ATTCACATCA CATGGATGCG GGTGAGACAG TGGCAAGGGA 60
 CATTGTTGG CACTGCTAT CGGCGGATTC GTCAGACGCC GCTTGTTGAG CCTTGCAGTG
 CTCGCGACGG CGAACGGCGA TCGGGAGGCC GCGCTTGCGT TACGCCACAG GCGCGCTCG
 CGCGCTCGA CGGGCTGCGC GCGGCGGACG CTGTTGCCCC CGCGCGACCG 120
 CGCGCGCGA AGCGCGCGA TGCGGACCG CGCGGATGAA TGGCGGACGT CGCGCGCGCG
 GACCGGCGC CGACCGCGC AGTCGTCATG CGCGGCGCGC CGCGGCGCGC CGCGCGCGCG 180
 GCGACCGCGC TGGAGGCGT CGCTCGCTG CTGGGTGGG GCTGCGACCG 185
 GCGCGCTCG ACTGGCGTCG AGTCGTCG AGCGAAAGCG CGCGGCGCGC CGCGCGCGCG
 40 GCGACCGCGC CGCGCGCGC CGACCGCGC CGCGCGCGC CGCGCGCGCG CGCGCGCGCG
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 240
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 300
 GACCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 360
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 420
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 480
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 540
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 600
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 660
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 720
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 780
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
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 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 840
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
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 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 960
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG
 GCGACCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 999

65 (2) INFORMATION FOR SEQ ID NO:41: DFRP

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

5 Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 6 10 15
 Arg Arg Lys Gly Arg⁷ Leu Ala Ala Leu Ala Ile Ala Asp Met Ala Ser
 20 24 28 32
 10 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 44 48
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 59 63
 15 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro
 65 70 75 80
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Asn
 85 90 95 98
 Pro Pro Pro Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
 100 105 110 115
 20 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Phe Val Gly Gly Phe Ser
 125 130 135 140
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Asn Phe Asp
 145 150 155 160
 Tyr Gly Ser Ala Leu Leu Ser Ile Thr Thr Gly Asp Pro Pro Phe Pro
 25 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 165 170 175 180
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 185 190 195 200
 30 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 215 220 225 230
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 245 250 255 260
 35 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 275 280 285 290
 Pro Asn Gly Glu Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 305 310 315 320
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 40 Thr Ala Asn Asn Pro Val Asp Iys Gly Ala Ala Lys Ala Leu Ala Glu
 325 330 335 340
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 350 355 360 365
 45 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 375 380 385 390
 Pro Thr Thr Pro Gln Arg Thr Leu Pro Ala
 395 400 405 410

50 (xii) INFORMATION FOR SEQ ID NO:42: TDB4

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO:42:

60	CGGGGGAGG ATGGTTTACCC CGGGGGATGCG ATTGGGGGGG TTTCGGGGCG	60
	CGGGGGGG CGGGGGGG CGGGGGGGG GGGGGGGGGG GGGGGGGGGG	120
	GCGCTCAATG TGTGGGGGGG ACCTTGCGGGG TTAAAGGAGA TAACTGGCTAT	180
	AGCTGTTAGG AGCTGTTAGG GATATGGGGG AGCTGGGGGG CTTGGGGGGG GATGGGGGG	240
	AGCTGTTAGG AGCTGTTAGG GATATGGGGG CGGGGGGGG GGGGGGGGGG	300
	CGCTGAGG GGGGGGGGGG AGCTGGGGGG CGGGGGGGGG GGGGGGGGGG	360
65	CGCTGAGG GGGGGGGGGG AGCTGGGGGG CGGGGGGGGG GGGGGGGGGG	420
	CGGGGGGGGG GGGGGGGGGG AGCTGGGGGG CGGGGGGGGG GGGGGGGGGG	480
	ACGGGGGGGG CGGGGGGGGG GGGGGGGGGG AGCTGGGGGG CGGGGGGGGG	540

GGCCGCACT AACGATGAGC CGGCGGTTGG CCAAGGCGG TGAACGAAAC TGCATGATGTC	600
TCAAGAAGC CGGCGGAGG CTCGAAACGCG GCGGCGGCG CCGCATCGCG CGCGCGTGG	660
GGATGCGTG GARACCTTCG ACCCTGTGCC TCGAAGGCGA CG	702

5

(i) INFORMATION FOR SEQ ID NO:43: TRN4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

15   Gly Asp Ser Phe Trp Ala Ala Asp Gin Met Ala Arg Gly Phe Val
      5          10          15
    Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Leu Gin
      20          25          30
20   His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
      35          40          45
    Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Lys Glu
      50          55          60
    Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
      65          70          75          80
    Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Glu Pro Pro Glu Pro Glu
      85          90          95
    Asn Phe Asp Pro Glu Gly Val Leu Gly Ile Tyr Arg Tyr His Ala
      100         105         110
    Ala Thr Glu Gin Arg Thr Asn Lys Asn Glu Ile Leu Ala Ser Gly Val
      115         120         125
    Ala Met Pro Ala Ala Leu Arg Ala Ala Glu Met Leu Ala Ala Glu Tyrp
      130         135         140
    Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Tyrp Gly Glu Leu Asn
      145         150         155         160
    Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
      165         170         175
    Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
      180         185         190
    Pro Val Ile Val Ser Asp Trp Met Arg Ala Val Pro Glu Glu Ile
      195         200         205
    Arg Pro Tyr Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
      210         215         220
    Gly Phe Ser Asp Thr Arg Ser Ala Gly Arg Arg Tyr Phe Asn Thr Asp
      225         230         235         240
    Ala Glu Ser Gin Val Gly Arg Gly Phe Gly Arg Gly Tyr Pro Gly Arg
      245         250         255
    Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
      260         265         270
    Leu Phe Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Lys Lys
      275         280         285

```

55 (ii) INFORMATION FOR SEQ ID NO:44: DPPD

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

65 (iv) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATTAAGATTA AGCTTACTCT CCTTAACTCT CGGCTTCTGGT TTTCCTCGCT CGGTTGCGG	60
CGGATGCGTG CGGCGGAGG CTCGAAACGCG GCGGCGGCG CCGCATCGCG CGCGCGTGG	120
GGATGCGTG CGGCGGAGG CTCGAAACGCG GCGGCGGCG CCGCATCGCG CGCGCGTGG	180

TACCCGCGG OCTGGTTTG GCAAGGTCG ATGCCAACCTT GGTTCACCGG CCCCCAGTTT
 TACTCTGATG GTCGACGGG CGTGTACCGG CTGGCGCGG CGGCGCCACG CGGTGGTTGC
 GGTGGGCGA TTCCCTCCA GCAACCCAAAC GTCGGCTG

5

(2) INFORMATION FOR SEQ ID NO:45; DPRD

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: protein

15

- (iii) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Lys	Leu	Lys	Phe	Ala	Arg	Leu	Ser	Thr	Ala	Ile	Leu	Gly	Cys	Ala
1															15
Ala	Ala	Leu	Val	Phe	Pro	Ala	Ser	Val	Ala	Ser	Ala	Asp	Pro	Pro	Asp
20															30
Pro	Mis	Gln	Pro	Asp	Met	Thr	Lys	Gly	Tyr	Cys	Pro	Gly	Gly	Arg	Trp
25															45
Gly	Phe	Gly	Asp	Ileu	Ala	Val	Cys	Asp	Gly	Glu	Lys	Tyr	Pro	Asp	Gly
30															55
Ser	Thr	Trp	His	Gln	Trp	Met	Gln	Thr	Trp	Phe	Thr	Gly	Pro	Gln	Phe
35															65
Tyr	Phe	Asp	Cys	Val	Ser	Gly	Gly	Glu	Pro	Ileu	Pro	Gly	Pro	Pro	Pro
40															75
Pro	Gly	Gly	Wif	Gly	Ala	Ile	Pro	Ser	Gln	Pro	Asp	Ala	Pro		
45															85
100															110

35

<210> SEQ ID NO:46

<211> P21

<212> DNA

<213> Artificial Sequence
<214> Description of Artificial Sequence: tri-fusion
protein DPF-MTI-MSL (designated Mch3If)

40

<222> {1}..{960}

45

cat	atg	cat	cac	cgt	cac	cat	gtc	ggc	ggc	gtc	att	sac		48
His	Met	His	His	His	His	His	Asp	Pro	Val	Asp	Ala	Val	Ile	Asn
5														15

50

acc	acc	ggc	aat	tac	ggg	cag	cta	gtt	gtt	ggc	ctc	acc	ggc		36
Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Ala	Ala	Leu	Asn	Ala	Thr	Asp	
20															39

55

ccg	ggg	acc	ggd	qua	cac	acc	ttt	ccg	gtt	ggc	ccg	ttt		144
Pro	Gly	Ala	Ala	Gln	Phe	Asn	Ala	Ser	Pro	Val	Ala	Gln	Ser	Tyr
35														45

60

tgc	ccg	aat	ttc	cch	ggc	ggc	ccg	cac	cot	cag	cgc	gtt	ggc		182
Leu	Arg	Asn	Phe	Leu	Ala	Ala	Phe	Pro	Pro	His	Arg	Ala	Ala	Met	Ala
55															60

65

ggc	ttt	ccg	aat	gtt	ccg	ccg	ggc	ccg	ccg	ttt	gtc		240	
Ala	Gln	Leu	Ile	Pro	Gly	Ala	Ala	Gln	Tyr	Ile	Gly	Leu	Val	
65														80

70

ggc	tcc	gtt	ggc	ggc	tcc	aa	ttt	ggc	ccg	ttt	ccg	ttt		288	
Gly	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr	Glu	Ileu	Met	Thr	Ile	Asn
65														95	

75

tac	ccg	tcc	ggg	ggc	gtc	aa	ttt	cat	ggc	ggc	atc	ccg	gtt		136	
Tyr	Gly	Asp	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln
100															110	

909 ggc tog ctt gag ggc gag cat cag gac atc gtt cgt gat ggc ttc 284
 Ala Ala Ser Leu Glu Ala Glu His Glu Ile Val Arg Asp Val Leu
 115 120 125
 5
 920 gca ggc ggt gac ttg tgg ggc ggc gca ggt tog gtc gct tgc cag ggc 432
 Ala Ala Gly Asp Phe Tyr Gly Gly Ala Gly Ser Val Ala Cys Glu Glu
 130 135 140
 10 ttc att acc cag itg ggc cgt aac ttc cag gtg atc tac gag cag god 480
 Phe Ile Thr Glu Leu Gly Arg Asn Phe Glu Val Ile Tyr Glu Glu Ala
 145 150 155 160
 15 gac pcc cat pms cmg amg pvg cmg gct gca ggc gac aac atg pcc cmx 528
 Asn Ala His Gly Glu Lys Val Glu Ala Ala Gly Asn Asn Met Ala Glu
 165 170 175
 20 acc gac agc gcc gtc ggc tcc aac tgg gcc act aat atg agc att ttc 576
 Thr Asp Ser Ala Val Gly Ser Ser Thr Ser Ser Met Ser Leu Ieu
 180 185 190
 25 gat gct cat atc cca caq trg ggc gca tcc cmg tog ggc gct gtc 624
 Asp Ala His Ile Pro Glu Leu Val Ala Ser Glu Ser Ala Phe Ala Ala
 195 200 205
 30 aag ggg ggg cts atg cgg ccc aac aag ahu ggt cmg gco ggg cmg ggg 672
 Lys Ala Gly Met Arg Glu Thr Ile Gly Glu Ala Glu Glu Ala Ala
 210 215 220
 35 gac tgg gct cag pcc ttt bac cgg ggg tgg tgg ggg gct ttc cgg 720
 Met Ser Ala Glu Ala Phe His Glu Gly Glu Ser Ser Ala Ala Phe Glu
 225 230 235 240
 40 gco gcc cat god cgg ttt gtt ggg god gco gcc gca gtc aac acc itg 768
 Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Ieu
 245 250 255
 45 tgg gat gtc ggg cmg pgg mat ctg ggt ggg god gco ggt acc cat gtg 816
 Leu Lys Val Ala Glu Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
 260 265 270
 50 gcc gco gat gct pgg god ggg tgg acc tat acc egg atc gat atc cat 864
 Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His
 275 280 285
 55 sac act ggc ggc cgg cgg aca aac ggc tgg taaacaaagcccgccggggaaag 917
 His Thr Gly Gly Arg Ser Ser Arg Ser Gly Phe Asp Ile His
 290 295
 <215> SEQ ID NO:47
 <216> 295
 <217> PPT
 <218> Artificial Sequences
 <219> Description of Artificial Sequence:tcti-fusion
 protein DPP-MTI-MSI (designated Mtb3f)
 60 Sis Met His
 1 5 10 15
 Thr Thr Cys Asn Tyr Glu Glu Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30
 65 Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Glu Ser Tyr
 35 40 45

Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
 50 55 60

5 Ala Glu Leu Glu Ala Val Pro Gly Ala His Glu Tyr Ile Gly Leu Val
 55 70 75 80

Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
 65 95 95

10 Tyr Glu Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 100 105 110

Ala Ala Ser Leu Glu Ala Glu His Glu Ala Ile Val Arg Asp Val Leu
 115 120 125

15 Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
 130 135 140

20 Phe Ile Thr Gln Leu Cys Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
 145 150 155 160

Asn Ala His Gly Gln Lys Val Glu Ala Ala Gly Asn Asn Met Ile Gln
 165 170 175

25 Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Ieu
 180 185 190

Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Ala
 195 205 205

30 Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
 210 215 220

35 Met Ser Ala His Ala Phe His Glu Glu Ser Ser Ala Ala Phe Gln
 225 230 235 240

Ala Ala His Ala Arg Phe Val Ile Ala Ala Ala Lys Val Asn Thr Ieu
 245 250 255

40 Ieu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
 255 265 270

Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His
 275 285 295

45 His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys
 290 295

50 <210> SEQ ID NO:48
 <211> 2169
 <212> DNA
 <213> Artificial Sequence
 <22> Description of Artificial Sequence:tetra-fusion
 protein DFV-MT1-MSL-MTCC2 (designated Mch7if)
 <22> (1)..(213)

cat atg cat ctc cat ctc cat ctc gat ccc gtq gac ggc gtu att aac 48
 His Met His His His His Asp Pro Val Asp Ala Val Ile Asn
 60 1 5 10 15

acc acc tgc aat tcc ggg cag gta gta got gog otc wac gog wog gat 94
 Thr Thr Cys Asn Tyr Gly Gin Val Val Ala Ala Ieu Asn Ala Thr Asp
 25 25 30

cog egg gtc gtc gca cag ttc aad gac tca cag gtc gtc cag tcc bat 144
 Pro Gly Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
 35 40 45

	rtg cgc aat ttc ctc gac gca eoc coa cct cag cgc gcr gcc aeg gco Leu Arg Asn Phe Leu Lys His Pro Pro Pro Glu Arg Ala Ala Met Ala	5	55	55	55	192
	gco cca ttp caa got gtg cog ggg ggc gca cag tac atc egc ott gce Ala Gln Leu Gln Ala Val Pro dly Lys Gln Tyr Ile Gly Leu Val	55	70	75	80	240
10	gag kog gtt gcc ggc tcc ttc tgc ead eas tat gag ctc atg eog att nat Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Gls Ieu Met Thr Ile Asn	85	90	95	95	268
15	cac cag ttc ggg gac gtc gao got cat ggc gco atg atc egd gct Cag Tyr Gln Phe Dly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln	105	105	110	110	336
20	gco gog kog ott eag gog gag dat wag gco atc gtr cgt gat ggc ktg Ala Ala Ser Leu Gln Ala Gln His Gln Ala Ile Val Arg Amp Val Ieu	115	120	125	125	384
25	gco gco ggt pac ttg tgg ggc ggc gco ggt tag gtg gct tcc cag ega Ala Ala Gly Asp Ser Trp Gly Gly Ser Val Ala Cys Glu Glu 130 135 140	130	135	140	140	432
30	tcc atc acc cag ttp gpc cgt aac ttc cag gtg atc tac gag cag gco Phe Ile Thr Gln Leu Gly Arg Asn Phe Glu Val Ile Tyr Glu Gln Ala 145 150 155 160	145	150	155	160	480
35	aac gtc can ggg cag gac gta cag get gco pdc aac aar atg pog oca Asn Ala His Gly Dly Val Gln Ala His Gly Asn Asn Met Ala Gln 165 170 175	165	170	175	175	528
40	aac gac aag gca gtc gyc tcc aeg tgg gco act axt atg atc gtc ott ttg Thr Asp Ser Ala Val Gly Ser Trp Ala Thr Ser Met Ser Leu Leu 185 188 190	185	188	190	190	576
45	gat gct cat atc cca eag ttg gtc gco tcc cag tag ggg ttt gct gco Asp Ala His Ile Pro Glu Leu Val Ala Ser Gln Ser Ala Dly Ala Ala 195 200 205	195	200	205	205	624
50	aag gcg ggg ctg atg cag ccc acg atc ggt cag gco gac ggg ggg ggg Lys Ala Dly Leu Met Arg His Thr Ile Gly Glu Ala Glu Gln Ala Ala 210 215 220	210	215	220	220	672
55	atg cgt gct cag ggg ttt cac cag ggg gac tag tag gco ggg ttt cag Met Ser Ala Ala Phe His Glu Glu Ser Ser Ala Ala Phe Glu 225 230 235 240	225	230	235	240	720
60	gco gco cat gco egs ttg gts gco ggg gco gco gac aac acc ttg Ala Ala His Ala Arg Phe Val His Ala Ala Lys Val Asn Thr Ieu 245 250 255	245	250	255	255	768
65	ttg gat gtc gco cag gog sat ctg ggt gco gco gco gct acc tat gtc Ieu Asp Val Ala Gln His Asn Ieu Gly Glu Ala Ala Gly Thr Tyr Val 260 265 270	260	265	270	270	816
70	gco gco gat gct gug gco gog tag acc tat acc ggg ttg gat atc atg Ala Ala Arg Ala Ala Ala Ala Ser Thr Tyr Thr Gly His Asp Ile Met 275 280 285	275	280	285	285	864
75	gat ttg egg ctt ttg act ccc gca gtc gat ttg acc aeg cga atg tat acc Asp Phe Gly Ieu Leu Pro Pro Glu Val Asn Ser Ser Arg Arg Met Tyr Ser 290 295 300	290	295	300	300	912

gtc gcc gca gag ttc act tcc ggc gca gtc tgg tat gga tgg gtc gtc 1098
 Val Ala Leu Thr Ser Ala Val Ser Tyr Gly Ser Val Val
 328 330 335 336
 5
 tgg aac ctg atc att ggg ccc tgg atc ggg ccc gca gca gca gca aac
 Ser Thr Ile Val Glu Pro Tyr Val Gly Pro Ala Ala Ala Ala Met
 340 345 350 355
 10 ggc gcc gca aac ccc tat gtc ggg tgg ctg gca gca gca aac gca gca
 Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Ile Ala Thr Ala Ala
 355 360 365 366
 15 ctc gca aag gaa acc gca acc ccc gca gca gca gca gca gca ttt
 Ile Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Glu Ala Phe
 370 375 380 385
 20 ggg aac ggg ttc ggg atg aac gtc ccc aca tcc ctc gca ggg gca aac
 Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn
 385 390 395 400
 25 aca aca ccc ttc aac tgg tcc gtc ggg aac att ctg ggg ccc aac aac
 Arg Ileu Arg Ileu Met Ser Ileu Val Ala Ala Asn Ile Leu Gly Ala Asn
 405 410 415 420
 30 aat ggg gca gtc gtc aac tac aac tat ggg ggg gca aac ggg gca gca
 Ser Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala
 425 430 435 440
 35 tgg ggg tgg ccc ccc ttc aac ccc aac ggg cca ggg aac ggg gca gca
 Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Glu Gly Thr Gly Pro Ala
 450 455 460 465
 40 ggg ccc ggg gca gca gca ggg ggg ggg aac ccc ggg gca ggg gca gca
 Gly Pro Ala Ala Ala Ala Ala Ala Thr Glu Ala Gly Ala Gly Ala
 465 470 475 480
 45 gtt ggg gat gca ccc ggg aac tgg gca ccc ggg ccc ccc aac atc ctg
 Val Ala Asp Ala Glu Ile Thr Leu Ala Glu Leu Pro Pro Gly Ile Leu
 485 490 495 500
 50 aac gac att ctg tcc gca trp gcu gca aac gac gac gat gat cog ctg sea tgg
 Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser
 500 505 510 515
 55 ggg ctg ttg ggg atc ggg tgg aac ccc aac cog ccc gtc ggg tcc got
 Gly Ileu Leu Gly Ile Ala Ser Thr Leu His Pro Glu Val Gly Ser Ala
 515 520 525 530
 60 cog ccc aca gtc aac aac aca atc ggg gca tgg gac gtc atc ggg
 Glu Pro Ile Val Ile Pro Thr Phe Ile Glu Glu Leu Asp Val Ile Ala
 530 535 540 545
 65 ctc tcc att gca tcc atc ggg aac ggc aac acc ggg ctg ggg aac aac
 Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
 550 555 560 565
 70 aac aca gca aca tgg ccc aac ggc atc tac ggg aac gtc gca ggg
 Asn Thr Ala Arg Pro Trp His Ile Glu Leu Tyr Gly Asn Ala Gly Gly
 565 570 575 580
 75 ctg ggg ctg ggg tgg ggg aat ccc aac atc ggg tgg ggg aac ggg gca
 Leu Gly Pro Thr Glu Gly His Pro Leu Ser His Ile Thr Asp Glu Pro
 585 590 595 600

gag ccc cac egg ggc ccc ttc ggg ggc egg ggc cog stg tcc ggc ggc
 Glu Pro Ala Trp Gly Pro Phe Gly Gly Ala Ala Ser Val Ser Ala Gly 1824
 595 600 605
 5 gtc ggc eac gca gca tta gtc gca gca ttg cog stg cog cac aac egg
 Val Gly His Ala Ala Ieu Val Gly Ala Leu Ser Val Pro His Ser Trp 1872
 610 615 620
 10 acc acc gcc gcc cog gag acc cog ctc gcr gtt cog gca aca ccc acc
 Thr Thr Ala Ala Pro Glu Ile Glu Leu Ala Val Glu Ala Thr Pro Thr 1930
 625 630 635 640
 15 rra aac tcc aac gac ggc ggc gac cog acc gac gca cta aac ggg abg cog
 Pro Ser Ser Ser Ala Gly Ala Arg Pro Thr Ala Leu Asn Gly Met Pro
 645 650 655
 20 gca ggc ctg ctc aac ggg abg cog gct ttg cog aac stg gcc gca aac
 Ala Gly Ieu Ieu Ser Gly Met Ala Ieu Ala Ser Ieu Ala Ala Arg Gly 2016
 650 655 660
 25 aac acc ggc ggt egg ggc acc cog gpc acc aac act gac gac gca
 Thr Thr Gly Gly Gly Thr Arg Gac Gly Thr Ser Thr Arg Gly Gln 2064
 675 680 685
 30 gag gac gcc cga aca ccc cog gta gtc att aac gag cag cog cog
 Glu Asp Gly Arg Lys Pro Val Val Ile Arg Glu Gln Pro Pro 2112
 690 695 700
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 Pro Gly Asn Pro Pro Arg
 705 710
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 45 <223> Description of Artificial Sequence:tetra-fusion
 protein DVV-MT1-MSH-MXCC2 (designated MtbVif)
 His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn
 1 6 10 15
 50 Thr Thr Cys Asn Tyr Gly Glu Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30
 Pro Gly Ala Ala Ala Glu Phe Asn Ala Ser Pro Val Ala Glu Ser Tyr
 35 40 45
 55 Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Glu Arg Ala Ala Met Ala
 50 55 60
 Ala Glu Ieu Glu Ala Val Pro Gly Ala Ala Glu Tyr Ile Gly Leu Val
 65 70 75 80
 Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Ieu Met Thr Ile Asn
 85 90 95
 60 Tyr Glu Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 100 105 110
 Ala Ala Ser Leu Glu Ala Glu His Glu Ala Ile Val Arg Asp Val Leu
 115 120 125
 65 Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Glu Glu
 130 135 140

Phe Ile Thr Glu Leu Gly Arg Asn Phe Glu Val Ile Tyr Glu Glu Ala
 145 156 155 160
 5 Asn Ala His Gly Glu Lys Val Glu Ala Ala Gly Asn Asn Met Ala Glu
 165 170 175
 Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Ieu
 180 185 190
 10 Asp Ala His Ile Pro Glu Leu Val Ala Ser Glu Ser Ala Phe Ala Ala
 195 200 205
 Lys Ala Gly Leu Met Arg His Thr Ile Gly Glu Ala Glu Glu Ala Ala
 210 215 220
 15 Met Ser Ala Glu Ala Phe His Glu Gly Glu Ser Ser Ala Ala Phe Glu
 225 230 235 240
 20 Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Ieu
 245 250 255
 Leu Asp Val Ala Glu Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
 260 265 270
 25 Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met
 275 280 285
 Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr Ser
 290 295 300
 30 Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp Gly
 305 310 315 320
 Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val
 325 330 335
 35 Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala Met
 340 345 350
 40 Ala Ala Ala Ala Thr Pro Tyr Val Glu Trp Leu Ala Ala Thr Ala Ala
 355 360 365
 Leu Ala Lys Glu Thr Ala Thr Glu Ala Arg Ala Ala Glu Ala Phe
 370 375 380
 45 Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn
 385 390 395 400
 Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Glu Asn
 405 410 415
 50 Ser Ala Ala Ile Ala Ala Thr Glu Ala Glu Tyr Ala Glu Met Trp Ala
 420 425 430
 55 Glu Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala
 435 440 445
 Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Glu Gly Thr Gly Pro Ala
 450 455 460
 60 Gly Pro Ala Ala Ala Ala Ala Thr Glu Ala Ala Glu Glu Ala Gly Ala
 465 470 475 480
 Val Ala Asp Ala Glu Ala Ala Thr Leu Ala Glu Leu Pro Pro Gly Ile Leu
 485 490 495
 65 Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser
 500 505 510

Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Glu Val Gly Ser Ala
 515 520 525

5 Glu Pro Ile Val Ile Pro Thr Pro Ile Gly Ala Leu Asp Val Ile Ala
 530 535 540

Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
 545 550 555 560

10 Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly
 565 570 575

Leu Gly Pro Thr Glu Gly His Pro Leu Ser Ser Ala Thr Asp Ala Pro
 580 585 590

15 Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
 595 600 605

Val Gly His Ala Ala Ile Val Gly Ala Leu Ser Val Pro His Ser Trp
 20 610 615 620

Thr Thr Ala Ala Pro Glu Ile Glu Leu Ala Val Glu Ala Thr Pro Thr
 625 630 635 640

25 Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
 645 650 655

Ala Gly Ile Leu Ser Gly Met Ala Ile Ala Ser Leu Ala Ala Arg Gly
 660 665 670

30 Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Glu
 675 680 685

35 Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
 690 695 700

Pro Gly Asn Pro Pro Arg
 705 710